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CROPS-LIVESTOCK INTERFACE FEED INVESTIGATION

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CROPS-LIVESTOCK INTERFACE FEED INVESTIGATION

Final Report

December 1, 2004

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Report December 1, 2004

1. Background

This project is a continuation of the Crops-Livestock Interface Project (20010329, RES46AD) which was initiated in December 2001 and which was reported in December 2002, September 2003, December 2003, March 2004 and August 2004. The initial work on the project was primarily analytical. A large number of samples of wheat, barley, oats, peas and forages were analyzed for their chemical content and the results have been transferred to a database where they can be used for economic modeling and variety selection. Work in the past year has shifted to utilization of crop varieties in ruminant and monogastrics species. For the next year's work, we propose to work on "picking winners" from the crop varieties we have worked on the last 3 years and develop 1) a slowly degradable starch variety of barley for beef and swine and 2) continue work on assessing flax fractions for their antibacterial properties. The proposed work plan for 2005 is included as an appendix to this report. In addition, we will continue chemical analysis of a smaller, focused number of grain, pulse and forage samples and will continue to incorporate these analyses and analyses from other projects into the feed database that has been created.

2. Abstract/ Executive Summary

The objectives of our work this year was to: 1) continue analysis of selected pea, barley and forage samples, 2) develop a method for determining in vivo starch degradation kinetics in pigs and determine the effect of starch degradation rate on nutrient utilization, 3) determine the effect of flax fractions on intestinal microbiology of the pig and 4) determine the potential for Saskatchewan cereal grains to support high efficiencies of nitrogen use in beef and dairy cattle.

During this year we have completed our analysis of 71 samples of pea, 28 samples of forages and 31 samples of barley. This information has been added to the feed database. The barley varieties were selected as likely candidates for slow starch degradation rates based on seed hardness. The pea and forage varieties were selected as part of ongoing breeding programs in the Crop Development Centre.

In Activity 1, 3 experiments were performed to determine an optimal methodology for determining starch degradation rates in pigs and to measure the starch degradation rates of the 31 barley samples analyzed for the feed database and to determine the effect of starch degradation rate on the efficiency of amino acid utilization in growing pigs. We have completed the first two of these experiments while the third is ongoing. We determined that a challenge sample of 25 g of glycemic carbohydrate was optimal and that white bread was the best control compared to a human diabetes test bar. Using this methodology we determined the starch degradation rate for 2 barley samples, 2 pea samples and corn. We found that Valier barley has a significantly lower rate of starch degradation than CDC Kendall. Both varieties of peas (CDC Mozart and Alfetta) had similar starch degradation rates and Corn had a starch degradation rate faster than the barley and pea samples tested.

In Activity 2, an ileal cannulation study was completed in which ileal and fecal microbial colonization was compared in grower pigs fed one of six diets: Diet 1: basal diet based on wheat, barley and soybean meal, Diet 2: basal diet plus 20% ground flax seed, Diet 3: basal diet plus 4% flax hulls, Diet 4: basal diet plus 18% hot water extracted flax seed, Diet 5: basa diet plus 8% flaxseed oil. Diet 6: basal diet with a standard antibiotic (tylan). Of note, flax hulls and flax oil (linseed oil) increased Lactobacillus counts in pig ileum in a manner similar to the antibiotic suggesting that theses fractions may have some probiotic value in improving pig health and performance.

3. Technical Report

The objective of this project is to apply detailed chemical characterization and basic nutritional principles for the selection of superior cereal grains, pulses, forages, for swine, poultry and cattle. To date we have analyzed over 700 samples of grains, pulses, oilseeds and forages. While some analysis of pea, barley and forage crops continued this year, we have concentrated in primarily two areas this year: 1) the development of a slowly degradable starch barley variety for pigs and cattle and 2) the assessment of the antibacterial properties of flax fractions.

3.1 Chemical Analysis of Pea Varieties

In the samples analyzed this year we noted significant differences between varieties for ether extract and acid detergent fibre (ADF). Variety 1287s-4 had a significantly higher ether extract than CDC 0102, CDC 103 and CDC 647-1. CDC 617-20 had the highest ADF content of all the pea varieties at 9.20%. A correlation analysis showed that the only significant correlations between chemical components were between starch and protein. These two components were negatively correlated with a correlation coefficient of -0.398. This suggests that selection for high protein varieties might result in a decrease in starch content. Table 1 shows the chemical analysis of the pea varieties.

Table 1. Crops Livestock Interface - Pea Summary - November 2004

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
04-237	C03P01B001	CDC Mozart	9.46	21.16	2.91	1.82	7.28	13.21	47.76
04-273	C03P01B002	CDC Mozart	9.88	23.50	2.58	2.03	7.43	12.75	52.63
04-239	C03P01C001	Eclipse	9.07	22.43	2.90	1.45	6.90	12.06	48.28
04-275	C03P01C002	Eclipse	9.58	22.11	2.68	1.57	7.37	17.49	51.69
04-242	C03P01E001	CDC 0101	9.10	22.18	2.75	1.47	7.67	12.55	45.25
04-278	C03P01E002	CDC 0101	9.56	23.44	2.48	1.35	7.67	11.31	50.40
04-243	C03P01F001	CDC 0102	9.26	21.58	2.78	0.92	7.38	14.50	47.65
04-279	C03P01F002	CDC 0102	9.73	22.87	2.65	1.61	7.50	14.35	52.99
04-244	C03P01G001	CDC 0103	9.04	23.00	2.88	1.01	7.01	14.35	45.48
04-280	C03P01G002	CDC 0103	9.59	22.62	2.63	1.60	6.98	18.72	53.18
04-245	C03P01I001	CDC 0105	9.13	21.86	2.88	1.43	7.77	12.82	47.78
04-281	C03P01I002	CDC 0105	9.40	23.87	2.61	1.64	7.82	16.82	51.35
04-246	C03P01L001	CDC 653-8	9.05	22.73	2.97	1.46	8.02	16.34	49.51
04-282	C03P01L002	CDC 653-8	9.79	23.24	2.62	1.22	8.23	13.38	52.34
04-249	C03P01K001	CDC 651-2	9.52	23.03	2.99	1.09	8.30	18.13	50.96
04-284	C03P01K002	CDC 651-2	9.10	21.97	3.03	1.56	7.38	12.79	48.08
04-250	C03P01M001	CDC 715s-4	9.13	22.58	2.87	1.52	6.56	11.96	47.41
04-285	C03P01M002	CDC 715s-4	9.26	23.99	2.90	1.14	7.27	14.63	50.76
04-251	C03P01Q001	617-20	9.24	20.40	3.32	1.68	9.14	14.77	48.98
04-286	C03P01Q002	617-20	9.34	22.95	3.13	1.62	9.26	13.39	47.66
04-252	C03P01V001	791-1	8.98	23.18	2.99	1.09	8.19	13.02	48.28
04-287	C03P01V002	791-1	9.43	24.84	2.98	1.53	8.79	13.88	46.69
04-238	C03P01CF001	Cutlass	9.27	21.94	2.89	1.53	7.62	13.39	45.90
04-274	C03P01CF002	Cutlass	9.65	22.18	2.59	1.62	8.60	13.63	51.83
04-259	C03P01CG001	985M-14	9.27	21.76	2.88	1.82	6.49	11.41	51.69
04-294	C03P01CG002	985M-14	8.87	24.72	2.88	1.80	7.85	16.28	49.66

04-260	C03P01CH001	985M-23	9.30	21.05	2.90	1.48	6.16	10.83	48.90
04-295	C03P01CH002	985M-23	9.29	23.34	2.40	2.18	7.95	19.65	45.82
04-261	C03P01CI001	985M-25	9.20	21.24	2.79	1.45	7.37	14.64	49.52
04-296	C03P01CI002	985M-25	9.28	23.67	2.71	1.75	7.47	15.52	46.12

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
04-262	C03P01CJ001	985M-27	9.21	22.22	2.85	1.58	7.38	11.47	48.02
04-297	C03P01CJ002	985M-27	9.19	23.15	2.75	1.16	7.66	15.30	47.03
04-263	C03P01CK001	985M-35	9.32	22.73	2.81	1.69	7.64	14.65	51.37
04-298	C03P01CK002	985M-35	9.08	22.85	2.74	1.25	7.38	16.84	45.98
04-254	C03P01CL001	996M-18	9.24	21.94	3.12	1.34	6.64	18.58	50.67
04-289	C03P01CL002	996M-18	9.37	23.79	2.88	1.67	7.75	19.65	51.03
04-255	C03P01CM001	1003M-4	9.30	22.42	2.94	1.84	7.89	15.94	51.98
04-290	C03P01CM002	1003M-4	9.37	22.93	2.87	1.51	7.83	19.44	52.22
04-256	C03P01CN001	1003M-45	9.37	23.06	2.92	1.83	7.49	13.15	48.14
04-291	C03P01CN002	1003M-45	9.35	22.68	2.91	2.03	7.65	16.35	50.85
04-253	C03P01CO001	1007M-6	8.97	20.95	2.86	1.66	7.78	12.71	50.78
04-288	C03P01CO002	1007M-6	9.20	24.19	2.82	1.53	7.85	13.84	51.23
04-258	C03P01CP001	1090M-47	9.17	21.31	2.94	1.92	7.30	12.83	51.80
04-293	C03P01CP002	1090M-47	9.33	22.77	2.95	2.09	7.55	19.27	45.94
04-257	C03P01CQ001	1287S-4	9.20	22.44	2.95	1.95	8.07	17.50	50.56
04-292	C03P01CQ002	1287S-4	9.43	23.18	2.8[illegible]	2.09	7.61	19.92	51.48
04-264	C03P01CR001	1308T-10	9.28	21.03	2.99	1.48	7.24	15.03	53.74
04-299	C03P01CR002	1308T-10	8.95	22.63	2.68	1.21	7.53	19.16	49.29
04-240	C03P02A001	Nitouche	9.37	20.72	3.06	1.24	8.37	17.35	47.86
04-276	C03P02A002	Nitouche	9.73	22.96	2.91	1.40	8.24	15.30	51.64
04-247	C03P02F001	CDC 672-1	8.71	25.18	3.28	1.27	7.62	17.45	46.17
04-248	C03P02E001	CDC 647-1	9.13	22.41	3.07	1.22	7.73	16.02	48.35
04-283	C03P02E002	CDC 647-1	9.28	23.49	3.02	1.21	8.71	13.95	51.83
04-267	C03P02AB001	1110M-8	9.33	23.45	3.23	1.53	7.27	12.84	46.47
04-302	C03P02AB002	1110M-8	9.19	26.01	2.71	1.14	7.38	15.14	43.14
04-268	C03P02A	1110M-	9.29	25.47	3.17	1.85	7.45	10.62	49.05

	C001	16							
04-303	C03P02A C002	1110M-16	9.27	26.18	2.85	1.65	7.48	12.03	45.55
04-265	C03P02A D001	1111M-2	9.05	24.89	3.03	1.61	7.71	14.56	48.04
04-300	C03P02A D002	1111M-2	8.94	24.99	2.79	1.28	7.50	18.55	44.95
04-266	C03P02A E001	1111M-8	9.07	23.20	2.95	1.55	8.62	17.72	50.43
04-301	C03P02A E002	1111M-8	8.76	24.15	2.81	1.38	8.94	18.25	45.46
04-270	C03P02A F001	1271S-11	9.28	23.84	2.89	1.96	7.13	14.52	51.79
Lab No.	**Sample ID**	**Variety**	Moist ure	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
04-305	C03P02A F002	1271S-11	8.89	27.58	2.95	1.54	8.46	12.27	43.11
04-269	C03P02A G001	1314T-4	9.07	22.28	2.90	1.80	7.55	11.49	51.47
04-304	C03P02A G002	1314T-4	8.80	25.90	2.86	1.59	8.49	13.37	39.88
04-241	C03P03A 001	CDC Acer	9.05	23.33	2.93	1.54	8.08	15.11	42.66
04-277	C03P03A 002	CDC Acer	9.79	24.10	2.54	1.50	8.71	14.34	52.05
04-271	C03P03H 001	1325T-1	9.43	24.44	2.93	1.58	7.62	13.29	49.62
04-306	C03P03H 002	1325T-1	9.47	24.39	2.62	1.54	8.21	13.62	45.16
04-272	C03P03I0 01	1325T-4	9.54	22.67	3.03	1.39	8.47	15.41	45.76
04-307	C03P03I0 02	1325T-4	9.52	23.95	2.63	1.62	8.44	15.03	44.98
		Mean	9.27	23.12	2.87	1.54	7.74	14.91	48.76
		Std. Dev.	0.245	1.378	0.178	0.272	0.609	2.446	2.930

CDC Mozart

Lab No.	Sample ID	Variety	Moist ure	CP_DM	ASH_ DM	EE_DM	ADF_ DM	NDF_ DM	STARCH _DM
04-237	C03P01B 001	CDC Mozart	9.46	21.16	2.91	1 82	7.28	13.21	47.76
04-273	C03P01B 002	CDC Mozart	9.88	23.50	2.58	2.03	7.43	12.75	52.63
		Mean	9.67	22.33	2.75	1.92	7.35	12.98	50.19
		Std. Dev.	0.30	1.65	0.23	0.15	0.11	0.33	3.44

Eclipse

Lab No.	Sample ID	Variety	Moist ure	CP_DM	ASH_ DM	EE_DM	ADF_ DM	NDF_ DM	STARCH _DM
04-239	C03P01C 001	Eclipse	9.07	22.43	2.90	1.45	6.90	12.06	48.28

04-275	C03P01C 002	Eclipse	9.58	22.11	2.68	1.57	7.37	17.49	51.69
		Mean	9.32	22.27	2.79	1.51	7.14	14.78	49.98
		Std. Dev.	0.36	0.22	0.15	0.09	0.33	3.84	2.41

CDC 0101

04-242	C03P01E 001	CDC 0101	9.10	22.18	2.75	1.47	7.67	12.55	45.25
04-278	C03P01E 002	CDC 0101	9.56	23.44	2.48	1.35	7.67	11.31	50.40
		Mean	9.33	22.81	2.61	1.41	7.67	11.93	47.82
		Std. Dev.	0.33	0.89	0.19	0.09	0.00	0.88	3.64

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy

CDC 0102

04-243	C03P01F0 01	CDC 0102	9.26	21.58	2.78	0.92	7.38	14.50	47.65
04-279	C03P01F0 02	CDC 0102	9.73	22.87	2.65	1.61	7.50	14.35	52.99
		Mean	9.49	22.23	2.72	1.27	7.44	14.42	50.32
		Std. Dev.	0.33	0.91	0.09	0.49	0.09	0.11	3.78

CDC 0103

04-244	C03P01G 001	CDC 0103	9.04	23.00	2.88	1.01	7.01	14.35	45.48
04-280	C03P01G 002	CDC 0103	9.59	22.62	2.63	1.60	6.98	18.72	53.18
		Mean	9.31	22.81	2.75	1.31	6.99	16.54	49.33
		Std. Dev.	0.39	0.27	0.18	0.42	0.02	3.09	5.44

CDC 0105

04-245	C03P01I0 01	CDC 0105	9.13	21.86	2.88	1.43	7.77	12.82	47.78
04-281	C03P01I0 02	CDC 0105	9.40	23.87	2.61	1.64	7.82	16.82	51.35
		Mean	9.26	22.86	2.74	1.54	7.80	14.82	49.57
		Std. Dev.	0.19	1.42	0.19	0.15	0.04	2.83	2.52

CDC 653-8

04-246	C03P01L0 01	CDC 653-8	9.05	22.73	2.97	1.46	8.02	16.34	49.51
04-282	C03P01L0 02	CDC 653-8	9.79	23.24	2.62	1.22	8.23	13.38	52.34
		Mean	9.42	22.99	2.79	1.34	8.12	14.86	50.92
		Std. Dev.	0.52	0.36	0.25	0.17	0.15	2.09	2.00

CDC 651-2

04-249	C03P01K001	CDC 651-2	9.52	23.03	2.99	1.09	8.30	18.13	50.96
04-284	C03P01K002	CDC 651-2	9.10	21.97	3.03	1.56	7.38	12.79	48.08
		Mean	9.31	22.50	3.01	1.33	7.84	15.46	49.52
		Std. Dev.	0.30	0.75	0.03	0.33	0.65	3.78	2.04

Lab No.	**Sample ID**	**Variety**	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy

CDC 715s-4

Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	STARCH_DM
04-250	C03P01M001	CDC 715s-4	9.13	22.58	2.87	1.52	6.56	11.96	47.41
04-285	C03P01M002	CDC 715s-4	9.26	23.99	2.90	1.14	7.27	14.63	50.76
		Mean	9.20	23.28	2.89	1.33	6.91	13.30	49.09
		Std. Dev.	0.09	1.00	0.02	0.27	0.50	1.89	2.37

CDC 617-20

04-251	C03P01Q001	617-20	9.24	20.40	3.32	1.68	9.14	14.77	48.98
04-286	C03P01Q002	617-20	9.34	22.95	3.13	1.62	9.26	13.39	47.66
		Mean	9.29	21.68	3.22	1.65	9.20	14.08	48.32
		Std. Dev.	0.07	1.81	0.14	0.04	0.08	0.98	0.93

CDC 791-1

04-252	C03P01V001	791-1	8.98	23.18	2.99	1.09	8.19	13.02	48.28
04-287	C03P01V002	791-1	9.43	24.84	2.98	1.53	8.79	13.88	46.69
		Mean	9.20	24.01	2.98	1.31	8.49	13.45	47.49
		Std. Dev.	0.31	1.17	0.01	0.31	0.43	0.61	1.13

Cutlass

04-238	C03P01CF001	Cutlass	9.27	21.94	2.89	1.53	7.62	13.39	45.90
04-274	C03P01CF002	Cutlass	9.65	22.18	2.59	1.62	8.60	13.63	51.83
		Mean	9.46	22.06	2.74	1.58	8.11	13.51	48.86
		Std. Dev.	0.27	0.17	0.22	0.07	0.69	0.17	4.19

985M-14

04-259	C03P01CG001	985M-14	9.27	21.76	2.88	1.82	6.49	11.41	51.69
04-294	C03P01CG002	985M-14	8.87	24.72	2.88	1.80	7.85	16.28	49.66
		Mean	9.07	23.24	2.88	1.81	7.17	13.85	50.67
		Std. Dev.	0.29	2.09	0.00	0.01	0.97	3.44	1.43

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy

985M-23

04-260	C03P01CH001	985M-23	9.30	21.05	2.90	1.48	6.16	10.83	48.90
04-295	C03P01CH002	985M-23	9.29	23.34	2.40	2.18	7.95	19.65	45.82
		Mean	9.29	22.19	2.65	1.83	7.05	15.24	47.36
		Std. Dev.	0.01	1.62	0.35	0.50	1.26	6.23	2.17

985M-25

04-261	C03P01CI001	985M-25	9.20	21.24	2.79	1.45	7.37	14.64	49.52
04-296	C03P01CI002	985M-25	9.28	23.67	2.71	1.75	7.47	15.52	46.12
		Mean	9.24	22.45	2.75	1.60	7.42	15.08	47.82
		Std. Dev.	0.06	1.72	0.05	0.21	0.08	0.62	2.41

985M-27

Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	STARCH_DM
04-262	C03P01CJ001	985M-27	9.21	22.22	2.85	1.58	7.38	11.47	48.02
04-297	C03P01CJ002	985M-27	9.19	23.15	2.75	1.16	7.66	15.30	47.03
		Mean	9.20	22.68	2.80	1.37	7.52	13.38	47.52
		Std. Dev.	0.02	0.66	0.07	0.30	0.20	2.71	0.70

985M-35

04-263	C03P01CK001	985M-35	9.32	22.73	2.81	1.69	7.64	14.65	51.37
04-298	C03P01CK002	985M-35	9.08	22.85	2.74	1.25	7.38	16.84	45.98
		Mean	9.20	22.79	2.78	1.47	7.51	15.74	48.67
		Std. Dev.	0.17	0.08	0.05	0.31	0.18	1.55	3.81

996M-18

04-254	C03P01CL001	996M-18	9.24	21.94	3.12	1.34	6.64	18.58	50.67
04-289	C03P01CL002	996M-18	9.37	23.79	2.88	1.67	7.75	19.65	51.03
		Mean	9.30	22.86	3.00	1.51	7.19	19.11	50.85
		Std. Dev.	0.09	1.31	0.17	0.23	0.78	0.76	0.25

1003M-4

04-255	C03P01CM001	1003M-4	9.30	22.42	2.94	1.84	7.89	15.94	51.98
04-290	C03P01CM002	1003M-4	9.37	22.93	2.87	1.51	7.83	19.44	52.22
		Mean	9.34	22.68	2.90	1.68	7.86	17.69	52.10
		Std. Dev.	0.05	0.36	0.05	0.24	0.04	2.48	0.18

1003M-45

04-256	C03P01CN001	1003M-45	9.37	23.06	2.92	1.83	7.49	13.15	48.14
04-291	C03P01CN002	1003M-45	9.35	22.68	2.91	2.03	7.65	16.35	50.85
		Mean	9.36	22.87	2.91	1.93	7.57	14.75	49.50
		Std. Dev.	0.01	0.27	0.01	0.14	0.11	2.26	1.91

1007M-6

04-253	C03P01CO001	1007M-6	8.97	20.95	2.86	1.66	7.78	12.71	50.78
04-288	C03P01CO002	1007M-6	9.20	24.19	2.82	1.53	7.85	13.84	51.23
		Mean	9.08	22.57	2.84	1.60	7.82	13.28	51.00
		Std. Dev.	0.16	2.29	0.03	0.09	0.05	0.80	0.32

1090M-47

04-258	C03P01CP001	1090M-47	9.17	21.31	2.94	1.92	7.30	12.83	51.80
04-293	C03P01CP002	1090M-47	9.33	22.77	2.95	2.09	7.55	19.27	45.94
		Mean	9.25	22.04	2.94	2.00	7.42	16.05	48.87
		Std. Dev.	0.12	1.03	0.01	0.12	0.18	4.55	4.14

1287S-4

Lab	Sample ID	Variety	Moistu	CP_D	ASH_D	EE_D	ADF_D	NDF_D	STARCH_

No.			re	M	M	M	M	M	DM
04-257	C03P01CQ001	1287S-4	9.20	22.44	2.95	1.95	8.07	17.50	50.56
04-292	C03P01CQ002	1287S4	9.43	23.18	2.89	2.09	7.61	19.92	51.48
		Mean	9.32	22.81	2.92	2.02	7.84	18.71	51.02
		Std. Dev.	0.16	0.52	0.04	0.09	0.32	1.71	0.65

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
1308T-10									
04-264	C03P01CR001	1308T-10	9.28	21.03	2.99	1.48	7.24	15.03	53.74
04-299	C03P01CR002	1308T-10	8.95	22.63	2.68	1.21	7.53	19.16	49.29
		Mean	9.12	21.83	2.84	1.34	7.39	17.09	51.52
		Std. Dev.	0.23	1.13	0.21	0.19	0.20	2.92	3.15
Nitouche									
04-240	C03P02A001	Nitouche	9.37	20.72	3.06	1.24	8.37	17.35	47.86
04-276	C03P02A002	Nitouche	9.73	22.96	2.91	1.40	8.24	15.30	51.64
		Mean	9.55	21.84	2.99	1.32	8.30	16.33	49.75
		Std. Dev.	0.25	1.58	0.11	0.11	0.10	1.45	2.67
CDC 647-1									
04-248	C03P02E001	CDC 647-1	9.13	22.41	3.07	1.22	7.73	16.02	48.35
04-283	C03P02E002	CDC 647-1	9.28	23.49	3.02	1.21	8.71	13.95	51.83
		Mean	9.20	22.95	3.05	1.22	8.22	14.99	50.09
		Std. Dev.	0.10	0.77	0.04	0.01	0.69	1.47	2.46
1110M-8									
04-267	C03P02AB001	1110M-8	9.33	23.45	3.23	1.53	7.27	12.84	46.47
04-302	C03P02AB002	1110M-8	9.19	26.01	2.71	1.14	7.38	15.14	43.14
		Mean	9.26	24.73	2.97	1.33	7.33	13.99	44.80
		Std. Dev.	0.10	1.81	0.37	0.27	0.08	1.63	2.35
1110M-16									
04-268	C03P02AC001	1110M-16	9.29	25.47	3.17	1.85	7.45	10.62	49.05
04-303	C03P02AC002	1110M-16	9.27	26.18	2.85	1.65	7.48	12.03	45.55
		Mean	9.28	25.82	3.01	1.75	7.47	11.32	47.30
		Std. Dev.	0.01	0.50	0.23	0.14	0.02	1.00	2.48

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
1111M-2									
04-265	C03P02AD001	1111M-2	9.05	24.89	3.03	1.61	7.71	14.56	48.04

04-300	C03P02AD002	1111M-2	8.94	24.99	2.79	1.28	7.50	18.55	44.95
		Mean	9.00	24.94	2.91	1.44	7.60	16.55	46.50
		Std. Dev.	0.08	0.07	0.17	0.23	0.15	2.83	2.19

1111M-8

Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	STARCH_DM
04-266	C03P02AE001	1111M-8	9.07	23.20	2.95	1.55	8.62	17.72	50.43
04-301	C03P02AE002	1111M-8	8.76	24.15	2.81	1.38	8.94	18.25	45.46
		Mean	8.92	23.68	2.88	1.46	8.78	17.99	47.94
		Std. Dev.	0.22	0.67	0.10	0.12	0.23	0.38	3.51

1271S-11

04-270	C03P02AF001	1271S-11	9.28	23.84	2.89	1.96	7.13	14.52	51.79
04-305	C03P02AF002	1271S-11	8.89	27.58	2.95	1.54	8.46	12.27	43.11
		Mean	9.08	25.71	2.92	1.75	7.79	13.40	47.45
		Std. Dev.	0.28	2.64	0.04	0.30	0.94	1.60	6.14

1314T-4

04-269	C03P02AG001	1314T-4	9.07	22.28	2.90	1.80	7.55	11.49	51.47
04-304	C03P02AG002	1314T-4	8.80	25.90	2.86	1.59	8.49	13.37	39.88
		Mean	8.93	24.09	2.88	1.70	8.02	12.43	45.68
		Std. Dev.	0.19	2.56	0.03	0.15	0.67	1.33	8.19

CDC Acer

04-241	C03P03A001	CDC Acer	9.05	23.33	2.93	1.54	8.08	15.11	42.66
04-277	C03P03A002	CDC Acer	9.79	24.10	2.54	1.50	8.71	14.34	52.05
		Mean	9.42	23.72	2.73	1.52	8.40	14.73	47.36
		Std. Dev.	0.53	0.54	0.28	0.03	0.45	0.54	6.64

Lab No.	**Sample ID**	**Variety**	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy

1325T-1

04-271	C03P03H001	1325T-1	9.43	24.44	2.93	1.58	7.62	13.29	49.62
04-306	C03P03H002	1325T-1	9.47	24.39	2.62	1.54	8.21	13.62	45.16

		Mean	9.45	24.42	2.78	1.56	7.91	13.45	47.39
		Std. Dev.	0.03	0.04	0.22	0.03	0.42	0.23	3.16

1325T-4

04-272	C03P03I001	1325T-4	9.54	22.67	3.03	1.39	8.47	15.41	45.76
04-307	C03P03I002	1325T-4	9.52	23.95	2.63	1.62	8.44	15.03	44.98
		Mean	9.53	23.31	2.83	1.50	8.46	15.22	45.37
		Std. Dev.	0.02	0.91	0.28	0.17	0.02	0.27	0.55

3.2 Barley Varieties

Valier barley is a slowly degradable starch type of barley which is highly desirable for feedlot diets. Unfortunately, Valier is an American variety and is not available to grow in Saskatchewan. We will therefore develop a Valier-like barley variety with good agronomic characteristics for Saskatchewan producers. Additionally, feeds with slow starch degradation rates fed to poultry have been shown to improve amino acid utilization and feed efficiency compared to feeds with rapidly degradable starch. A Valier-like barley variety should be desirable for use in swine and poultry diets.

As a first step in this project, 31 varieties of barley were analyzed this year in preparation for measurement of starch degradation rates of these varieties in pigs and cattle (Table 2). These barley's were selected on the basis of chemical composition and seed hardness to provide a large selection of barley varieties with differing starch degradation properties.

Table 2. Crops Livestock Interface - Barley Summary - November 2004

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
04-213	C03B11A0 01	Unregistered	10.51	14.52	2.30	2.05	4.03	23.2 0	4440.5
04-214	C03B15A0 01	Unregistered	11.25	14.63	2.40	2.03	4.23	20.3 7	4417.5
04-215	C03B01D0 01	CDC Dolly	10.93	14.35	2.42	1.86	6.77	20.9 2	4409.1
04-216	C03B26A0 01	Unregistered	11.32	15.09	2.41	1.97	6.76	23.3 3	4446.8
04-217	C03B15A0 02	Unregistered	10.53	15.32	2.43	1.95	5.84	16.8 8	4440.8
04-218	C03B09A0 01	Valier	10.46	14.58	2.53	2.08	5.79	17.3 9	4408.0
04-219	C03B23A0 01	Unregistered	9.36	18.25	2.11	2.96	2.03	21.9 4	4542.1
04-220	C03B27A0 01	Condor	10.64	16.82	1.88	2.42	2.43	13.6 6	4449.7
04-221	C03B03A0 01	CDC McGuire	10.55	15.98	1.84	2.24	2.62	14.2 5	4464.9
04-222	C03B19A0 01	Unregistered	12.17	17.10	2.05	2.82	2.08	21.6 5	4457.5
04-223	C03B15A0 03	Unregistered	12.34	16.38	2.03	2.81	2.51	11.8 0	4413.0
04-224	C03B15A0 04	Unregistered	11.99	14.91	1.82	2.31	2.50	11.2 1	4460.2
04-225	C03B16B0 01	Unregistered	8.98	13.55	2.08	2.16	2.85	14.0 1	4514.8
04-226	C03B09B0 01	Unregistered	8.44	13.78	2.31	2.64	1.17	19.1 5	4353.2
04-227	C03B01E0 01	CDC Dawn	8.45	12.13	2.09	2.70	0.99	12.3 8	4323.3
04-228	C03B22A0 01	Unregistered	9.17	17.77	1.86	2.67	3.12	21.0 3	4465.3
04-229	C03B05A0 01	Unregistered	11.74	18.14	1.99	2.76	1.81	20.5 4	4402.2
04-230	C03B20A0 01	CDC Alamo	10.39	16.72	2.07	3.30	2.58	22.1 5	4486.1
04-231	C03B16A0 01	CDC Gainer	8.87	10.99	2.19	2.47	2.77	14.1 7	4428.8
04-232	C03O11A0 01	Unregistered	10.18	15.41	3.45	4.02	17.3 2	43.0 9	4425.9
04-233	C03O09A0 01	Unregistered	7.98	15.81	3.71	7.42	16.4 1	32.4 4	4817.0
04-234	C03O10A0 01	AC Assiniboia	7.63	13.08	4.21	5.61	15.3 0	34.6 6	4487.2
04-235	C03O10H0 01	AC Morgan	7.27	12.20	3.18	4.35	14.6 9	31.0 6	4478.6
04-236	C03O10D0 01	CDC Dancer	7.84	13.35	3.32	4.29	12.9 0	28.7 6	4491.2
04-308	C03B01B0 01	AC Metcalfe	9.52	11.07	2.58	2.34	5.27	15.5 3	4193.7
04-309	C03B03C0 01	Unregistered	9.45	12.66	2.75	2.50	6.65	18.8 4	4312.9

04-310	C03B29A001	Unregistered	9.49	15.46	2.20	2.50	5.56	19.60	4348.2
04-311	C03B01F001	CDC Helgason	9.56	12.46	2.63	2.65	5.95	17.97	4355.8
04-312	C03B01D002	CDC Dolly	9.77	12.25	2.43	2.22	5.39	20.78	4261.0
04-313	C03B01G001	CDC Bold	9.88	11.33	2.65	2.39	5.28	15.66	4283.5
04-314	C03B09A002	Valier	9.85	12.08	2.62	2.42	5.76	18.11	4292.2
		Mean	9.89	14.46	2.47	2.87	5.79	20.53	4421.7
		Std. Dev.	1.338	2.111	0.573	1.180	4.623	7.163	108.8

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Gross Energy
04-213	C03B11A001	Unregistered	10.51	14.52	2.30	2.05	4.03	23.20	4440.5
04-214	C03B15A001	Unregistered	11.25	14.63	2.40	2.03	4.23	20.37	4417.5
04-215	C03B01D001	CDC Dolly	10.93	14.35	2.42	1.86	6.77	20.92	4409.1
04-216	C03B26A001	Unregistered	11.32	15.09	2.41	1.97	6.76	23.33	4446.8
04-217	C03B15A002	Unregistered	10.53	15.32	2.43	1.95	5.84	16.88	4440.8
04-218	C03B09A001	Valier	10.46	14.58	2.53	2.08	5.79	17.39	4408.0
04-219	C03B23A001	Unregistered	9.36	18.25	2.11	2.96	2.03	21.94	4542.1
04-220	C03B27A001	Condor	10.64	16.82	1.88	2.42	2.43	13.66	4449.7
04-221	C03B03A001	CDC McGuire	10.55	15.98	1.84	2.24	2.62	14.25	4464.9
04-222	C03B19A001	Unregistered	12.17	17.10	2.05	2.82	2.08	21.65	4457.5
04-223	C03B15A003	Unregistered	12.34	16.38	2.13	2.81	2.51	11.80	4413.0
04-224	C03B15A004	Unregistered	11.99	14.91	1.82	2.31	2.50	11.21	4460.2
04-225	C03B16B001	Unregistered	8.98	13.55	2.08	2.16	2.85	14.01	4514.8
04-226	C03B09B001	Unregistered	8.44	13.78	2.31	2.64	1.17	19.15	4353.2
04-227	C03B01E001	CDC Dawn	8.45	12.13	2.09	2.70	0.99	12.38	4323.3
04-228	C03B22A001	Unregistered	9.17	17.77	1.86	2.67	3.12	21.03	4465.3
04-229	C03B05A001	Unregistered	11.74	18.14	1.99	2.76	1.81	20.54	4402.2
04-230	C03B20A001	CDC Alamo	10.39	16.72	2.07	3.30	2.58	22.15	4486.1
04-231	C03B16A001	CDC Gainer	8.87	10.99	2.19	2.47	2.77	14.17	4428.8

04-308	C03B01B001	AC Metcalfe	9.52	11.07	2.58	2.34	5.27	15.53	4193.7
04-309	C03B03C001	Unregistered	9.45	12.66	2.75	2.50	6.65	18.84	4312.9
04-310	C03B29A001	Unregistered	9.49	15.46	2.20	2.50	5.56	19.60	4348.2
04-311	C03B01F001	CDC Helgason	9.56	12.46	2.63	2.65	5.95	17.97	4355.8
04-312	C03B01D002	CDC Dolly	9.77	12.25	2.43	2.22	5.39	20.78	4261.0
04-313	C03B01G001	CDC Bold	9.88	11.33	2.65	2.39	5.28	15.66	4283.5
04-314	C03B09A002	Valier	9.85	12.08	2.62	2.42	5.76	18.11	4292.2
		Mean	10.22	14.55	2.26	2.43	3.95	17.94	4398.9
		Std. Dev.	1.11	2.21	0.28	0.35	1.87	3.67	83.17

3.3 Forage Varieties

Twenty-eight varieties of forage were analyzed this year and are shown in Table 3. Although there is no planned work on forages this year, it is envisioned that Dr. Yu, the new SAFRR scientist will investigate forage varieties in the future.

Crops Livestock Interface - SFC Forage Summary - November 2004

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Lignin
03-261	S02AF03H001	Magnum III Wet	5.47	14.70	9.57	3.88	30.60	41.68	7.45
03-262	S02AF03H002	Magnum III Wet	6.00	14.03	9.69	3.16	29.54	35.62	6.24
03-263	S02AF04E001	Hornet	5.68	16.56	9.94	3.03	27.52	37.52	6.48
03-264	S02AF04E002	Hornet	5.77	12.67	9.32	3.10	25.81	35.30	6.28
03-265	S02AF03I001	Survivor	5.64	12.36	8.66	3.06	26.43	36.05	6.87
03-266	S02AF03I002	Survivor	5.75	15.97	9.50	3.12	28.80	38.67	7.25
03-267	S02AF03J001	Gala	5.67	16.35	10.01	3.08	26.50	36.60	6.40
03-268	S02AF03J002	Gala	5.79	13.60	9.39	2.92	25.39	34.03	6.91
03-269	S02AF02F001	Spredor III	5.53	14.49	10.35	2.61	34.33	40.88	6.98
03-270	S02AF02F002	Spredor III	5.55	12.23	9.03	2.80	30.37	36.05	6.49
03-271	S02AF01F001	54V54	5.78	16.04	10.26	3.24	31.86	35.65	6.65
03-272	S02AF01F002	54V54	5.83	14.26	8.86	2.53	30.32	35.64	7.05
03-273	S02AF03K001	AC Longview	5.74	14.63	10.41	2.99	32.16	40.01	8.58
03-274	S02AF03K002	AC Longview	5.76	14.97	8.37	2.43	30.16	38.12	8.55
03-275	S02AF02G001	Runner	5.62	15.00	9.75	2.18	36.02	45.14	7.03
03-276	S02AF02G002	Runner	5.69	15.09	8.68	2.46	32.39	39.65	7.14
03-277	S02AF01G001	PS2065MF	5.91	15.80	10.57	2.78	31.50	37.41	6.29
03-278	S02AF01G002	PS2065MF	5.65	14.57	8.47	2.07	30.24	34.77	7.05
03-279	S02AF03L001	PS8925MF	5.67	15.36	10.07	2.62	32.75	39.83	8.33
03-280	S02AF03L002	PS8925MF	5.57	15.32	8.72	2.33	32.57	35.94	9.33
03-281	S02AF01H001	AC Grazeland	5.30	14.61	9.94	2.36	34.13	41.06	7.11
03-282	S02AF01H002	AC Grazeland	5.39	15.82	8.69	2.55	30.54	36.33	7.23

03-283	S02AF01A001	Beaver	5.56	16.27	8.49	2.65	30.56	36.77	6.51
03-284	S02AF01A002	Beaver	5.87	16.62	8.67	2.72	28.35	32.63	9.34
03-285	S02TF00A001	Courtenay	4.82	11.97	6.48	4.28	31.61	54.09	5.00
03-286	S02TF00A002	Courtenay	4.93	15.73	7.89	3.07	30.73	51.05	3.30
Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Lignin
03-287	S02TM00C001	Jolliette	4.55	9.41	4.83	3.02	33.68	60.57	4.52
03-288	S02TM00B001	Climax	4.69	9.02	4.92	2.98	34.96	60.13	4.71
		Mean	5.54	14.41	8.91	2.86	30.71	40.26	6.82
		Std. Dev.	0.367	1.956	1.445	0.471	2.756	7.394	1.348

Magnum III Wet

Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	LIG_DM
03-261	S02AF03H001	Magnum III Wet	5.47	14.70	9.57	3.88	30.60	41.68	7.45
03-262	S02AF03H002	Magnum III Wet	6.00	14.03	9.69	3.16	29.54	35.62	6.24
		Mean	5.73	14.36	9.63	3.52	30.07	38.65	6.84
		Std. Dev.	0.37	0.48	0.08	0.51	0.75	4.28	0.86

Hornet

Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	LIG_DM
03-263	S02AF04E001	Hornet	5.68	16.56	9.94	3.03	27.52	37.52	6.48
03-264	S02AF04E002	Hornet	5.77	12.67	9.32	3.10	25.81	35.30	6.28
		Mean	5.72	14.62	9.63	3.07	26.67	36.41	6.38
		Std. Dev.	0.07	2.75	0.44	0.05	1.21	1.57	0.15

Survivor

03-265	S02AF03I001	Survivor	5.64	12.36	8.66	3.06	26.43	36.05	6.87
03-266	S02AF03I002	Survivor	5.75	15.97	9.50	3.12	28.80	38.67	7.25
		Mean	5.70	14.16	9.08	3.09	27.62	37.36	7.06
		Std. Dev.	0.08	2.55	0.60	0.04	1.67	1.85	0.27

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Lignin

Gala

03-267	S02AF03J001	Gala	5.67	16.35	10.01	3.08	26.50	36.60	6.40
03-268	S02AF03J002	Gala	5.79	13.60	9.39	2.92	25.39	34.03	6.91
		Mean	5.73	14.97	9.70	3.00	25.95	35.31	6.65
		Std. Dev.	0.08	1.94	0.44	0.12	0.78	1.82	0.36

Spreador III

03-269	S02AF02F001	Spredor III	5.53	14.49	10.35	2.61	34.33	40.88	6.98
03-270	S02AF02F002	Spredor III	5.55	12.23	9.03	2.80	30.37	36.05	6.49
		Mean	5.54	13.36	9.69	2.70	32.35	38.47	6.73
		Std. Dev.	0.01	1.60	0.93	0.14	2.80	3.42	0.35

54V54

03-271	S02AF01F001	54V54	5.78	16.04	10.26	3.24	31.86	35.65	6.65
03-272	S02AF01F002	54V54	5.83	14.26	8.86	2.53	30.32	35.64	7.05
		Mean	5.80	15.15	9.56	2.89	31.09	35.64	6.85
		Std. Dev.	0.04	1.26	0.99	0.50	1.09	0.01	0.28

AC Longview

03-273	S02AF03K001	AC Longview	5.74	14.63	10.41	2.99	32.16	40.01	8.58
03-274	S02AF03K002	AC Longview	5.76	14.97	8.37	2.43	30.16	38.12	8.55
		Mean	5.75	14.80	9.39	2.71	31.16	39.07	8.56
		Std. Dev.	0.02	0.24	1.44	0.40	1.41	1.33	0.02

Runner

03-275	S02AF02G001	Runner	5.62	15.00	9.75	2.18	36.02	45.14	7.03
03-276	S02AF02G002	Runner	5.69	15.09	8.68	2.46	32.39	39.65	7.14
		Mean	5.66	15.04	9.21	2.32	34.20	42.40	7.08
		Std. Dev.	0.05	0.06	0.75	0.20	2.57	3.88	0.08

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Lignin
PS2065MF									
Lab No.	Sample ID	Variety	Moisture	CP_DM	ASH_DM	EE_DM	ADF_DM	NDF_DM	LIG_DM
03-277	S02AF01G001	PS2065MF	5.91	15.80	10.57	2.78	31.50	37.41	6.29
03-278	S02AF01G002	PS2065MF	5.65	14.57	8.47	2.07	30.24	34.77	7.05
		Mean	5.78	15.19	9.52	2.42	30.87	36.09	6.67
		Std. Dev.	0.18	0.87	1.49	0.50	0.89	1.87	0.53
PS8925MF									
03-279	S02AF03L001	PS8925MF	5.67	15.36	10.07	2.62	32.75	39.83	8.33
03-280	S02AF03L002	PS8925MF	5.57	15.32	8.72	2.33	32.57	35.94	9.33
		Mean	5.62	15.34	9.39	2.47	32.66	37.89	8.83
		Std. Dev.	0.07	0.03	0.95	0.20	0.13	2.75	0.71
AC Grazeland									
03-281	S02AF01H001	AC Grazeland	5.30	14.61	9.94	2.36	34.13	41.06	7.11
03-282	S02AF01H002	AC Grazeland	5.39	15.82	8.69	2.55	30.54	36.33	7.23
		Mean	5.34	15.22	9.31	2.45	32.34	38.70	7.17
		Std. Dev.	0.06	0.86	0.89	0.13	2.54	3.34	0.09
Beaver									
03-283	S02AF01A001	Beaver	5.56	16.27	8.49	2.65	30.56	36.77	6.51
03-284	S02AF01A002	Beaver	5.87	16.62	8.67	2.72	28.35	32.63	9.34
		Mean	5.71	16.44	8.58	2.69	29.45	34.70	7.93
		Std. Dev.	0.22	0.25	0.13	0.05	1.57	2.92	2.00
Courtenay									
03-285	S02TF00A001	Courtenay	4.82	11.97	6.48	4.28	31.61	54.09	5.00
03-286	S02TF00A002	Courtenay	4.93	15.73	7.89	3.07	30.73	51.05	3.30
		Mean	4.88	13.85	7.19	3.67	31.17	52.57	4.15
		Std. Dev.	0.08	2.66	0.99	0.86	0.62	2.15	1.21

Lab No.	Sample ID	Variety	Moisture	Crude Protein	Ash	Ether Extract	ADF	NDF	Lignin
Jolliette									
03-287	S02TM00C001	Jolliette	4.55	9.41	4.83	3.02	33.68	60.57	4.52
Climax									
03-288	S02TM00B001	Climax	4.69	9.02	4.92	2.98	34.96	60.13	4.71

3.4 Prairie Feed Resource Centre Grain & Forage Database

The results of the analyses for the entire Crops-Livestock Interface project have been compiled and transferred to the PFRC Grain & Forage Database where they are accessible by designated end users.

3.5 Starch Degradation Rates of Saskatchewan Feeds in Growing Pigs

During the last 7 months we have completed 2 studies on starch degradation rates of SK crops in growing pigs. Tanya Warren has been recruited as a M.Sc. student on this project and will complete her research in 2005. The two studies are outlined below.

3.5.1 Development of a method for assessing in vivo starch degradation rates in pigs

Objective:

1) To determine the best dose of starch and best control feed for starch kinetic determination in pigs

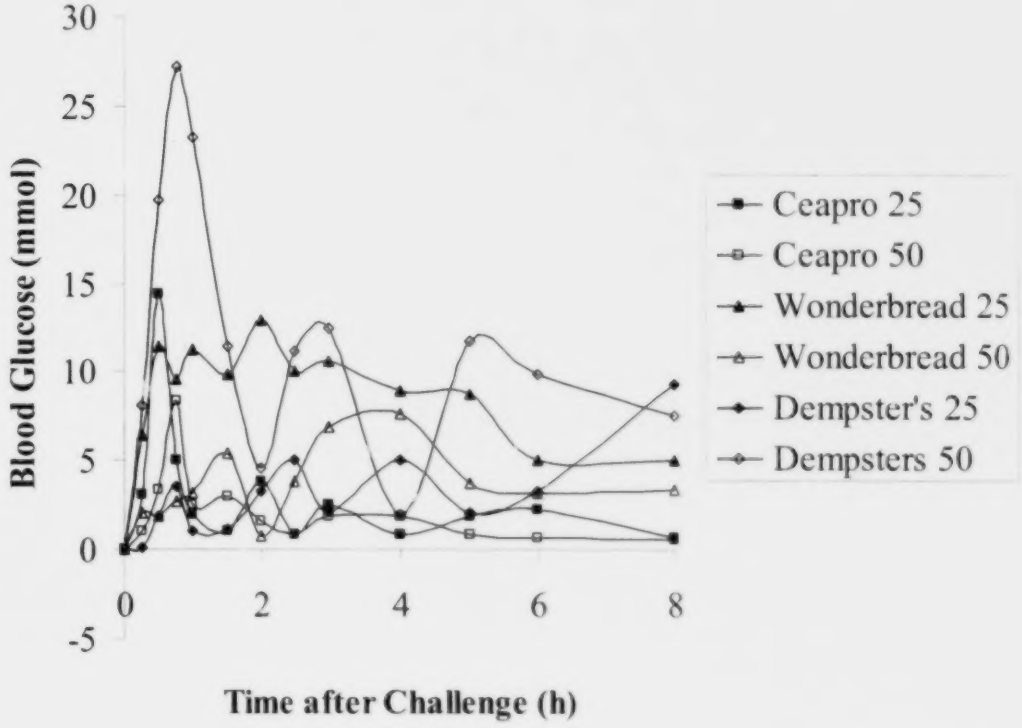
6 Weanling pigs (barrows); 21 days of age; closely matched in weights.

Experimental protocol

Weanling pigs (6 barrows; 21 days of age) were used in the experiment. The pigs were fasted for a 12 h period overnight. In the morning the pigs were given challenge doses of 25 or 50 g of glycemic carbohydrate using three challenge feeds: Ceapro Accutest, and 2 types of white bread. All pigs were given the same sample and sample size each day. Blood samples were taken at -1, -0.5, 0, .25, .5, .75, 1, 1.5, 2, 2.5, 3, 4, 5, 6 and 8 hours post-challenge and blood glucose will be taken using a Hemocue glucose meter. After the last blood sample, pigs were then fed ad libitum until 9 pm when the feed was removed and the pigs fasted until the next days testing. Sampling was not done on weekends.

The results are shown in Figure 1. The Demster's white bread 50 g challenge dose gave the most consistent results and was chosen as the control for all future experiments.

Figure 1. Blood glucose response after a 25 or 50 g dose of glycemic carbohydrate from 3 products.



3.5.2 Starch degradation rates of selected Saskatchewan crops

Hypothesis

The kinetics of starch digestion of grains and pulses in pigs varies significantly with intrinsic factors (starch type, association of starch with protein, non-starch polysaccharides) and extrinsic factors (processing including particle size and hydrothermal treatment). Differences in starch digestion kinetics will significantly affect the protein and energy metabolism of pigs.

Objectives:

1) Measure the kinetics of starch digestion and glycemic index of diverse varieties of barley, wheat, durum wheat, oats, peas and corn in growing pigs.
2) Develop improved in vitro starch kinetic assays that correlate well with in vivo starch kinetics in pigs.
3) Demonstrate the effect of starch degradability rate on amino acid and energy utilization in growing pigs.

4) In collaboration with plant breeders in the Crop Development Centre at the University of Saskatchewan, develop improved feeding varieties of barley, oats and peas based on their starch degradability characteristics.

Animals

8 Weanling pigs (barrows); 21 days of age; closely matched in weights.

Experimental protocol

Experimental Feeds

- Ceapro Accuscreen was used as a control feed (10 cookies for a total of 50 g glycemic carbohydrate).
- Samples of corn, CDC Kendall barley, Valier barley, CDC Mozart peas and Alfetta peas were be used as test samples. The feeds were ground to approximately 900 um particle size.
- Bars containing exactly 50 g of glycemic carbohydrate (Total starch x 0.9 + free glucose) were prepared by moistening the ground grains to give approximately 35% water, shaping the moistened barley into a bar 4 °C overnight.

Plasma glucose response

- Pigs were fasted overnight for exactly 15 hours (5 pm to 8am)
- At 8am an initial blood glucose reading was taken from all pigs
- Pigs were then be fed the control or test feed which was consumed in less than 5 minutes.
- Blood glucose was measured at 15, 30, 45, 60, 90, 120, 150 180 minutes after the bars were consumed.
- Pigs were then given ad libitum access to feed until 5pm.
- All samples were done in duplicate.
- Each pig received the AccuScreen control on Wedneday of every week with test feeds being fed Mon, Tue, Thu and Fri.

Analysis of results:

Blood glucose was plotted against time and the total area under the glucose response curve for the AccuScreen challenge was calculated by the method of Wolever et al. (1991). The area under the glucose response curve for each pig at each sampling time was then divided by the total area under the curve for the AccuScreen challenge using the formula:

$$G_{ijk} = T_{ijk}/A_{i,180,AccuScreen,k}$$

Where G_{ijkl} = Relative glycemic response above baseline for pig i at time j, for sample k in week l.

T_{ijkl} = Cumulative area under the glucose response curve for pig i, at time j, for sample k in week l.

$A_{i,180,AccuScreen,k}$ = Total area under the glucose response curve for pig I at time 180 minuts for the AccuScreen challenge for in week l

Linear regression analysis was performed using SPSS (Version 12.0) with intercepts set to 0.

Results:

Figure 2 shows blood glucose levels observed in the pigs during the 3 hour period after the challenge. Figure 3 shows the cumulative appearance of blood glucose relative to the control. Table 4 shows the slope of the regression lines and the glycemic indexes of the feeds relative to AccuScreen. The relative values agree well with the previous study. However, AccuScreen has a lower glycemic index than white bread so that using AccuScreen as a standard resulted in lower absolute glycemic indexes. The rate of g ucose appearance was lowest for CDC Mozart peas. Valier barley had a significantly lower rate of starch appearance than Kendall barley.

Based on these results we will perform an experiment to determine the effect of starch degradation rate on lysine requirements in growing pigs using Valier and Kendall barley as sources of slowly and rapidly digestible starch.

Figure 2. Blood glucose values after a challenge with 50 g of glycemic carbohydrate.

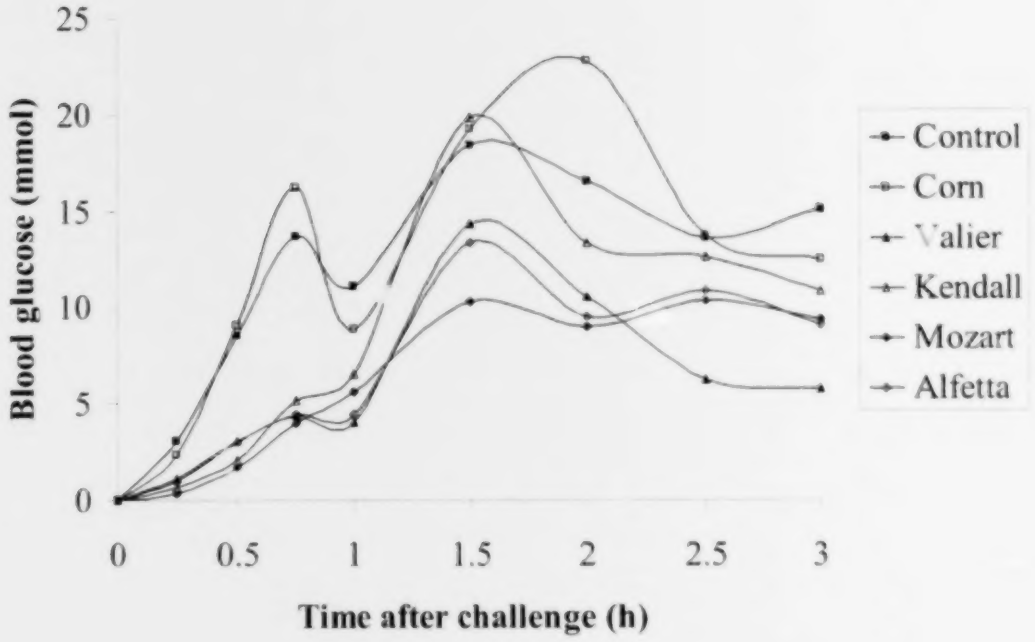


Figure 3. Cumulative glycemic response of pigs fed 50 g of glycemic carbohydrate relative to Accuscreen.

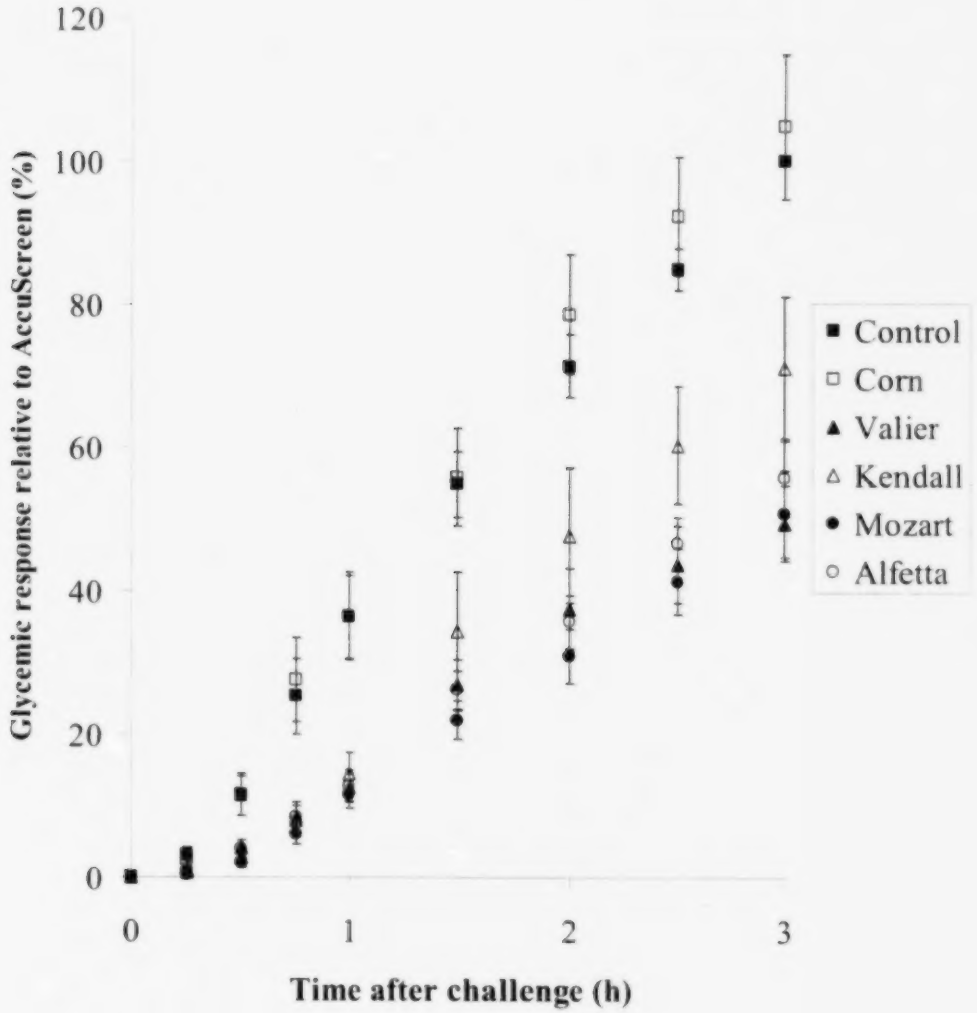


Table 1. Linear regression of cumulative glucose response and glycemic index of samples relative to AccuScreen.

Sample	Slope*	r^2	Glycemic Index
AccuScreen	34.17	.99	100
Corn	36.32	.99	104.8
Kendall	22.78	.95	71.1
Valier	16.83	.97	49.4
Mozart	15.70	.96	50.7
Alfetta	17.75	.97	55.6

*Intercept was set to 0 for all regression equations.

The Canadian swine industry currently depends heavily on antibiotics for disease prevention and growth promotion. Considering that the swine industry's use of antibiotics is likely to be heavily restricted in the future, effective alternatives need to be discovered. It is hypothesized that the unique chemical composition of Saskatchewan feed ingredients may give it antimicrobial properties. Also, selection of new varieties of feed ingredients should give consideration to the effect of changes in variety composition on animal health and food safety.

Through a collaboration with Drs. R.T. Zijlstra, M.D. Drew and A.G. Van Kessel funding has been obtained from several sources including Flax Council of Canada, SaskPork, ADF Projects fund and the Crops-livestock interface (CLI) to support evaluation of the nutritional and microbiological properties of flaxseed ands its fractions compared with inclusion of a dietary antibiotic in swine. CLI funding has been used specifically to use of molecular profiling techniques to inventory intestinal bacterial and quantify specific organisms.

3.6 Gut microbiology and feed ingredients

The ileal cannulation study has been completed in which ileal and fecal microbial colonization was compared in grower pigs fed one of six diets: Diet 1: basal diet based on wheat, barley and soybean meal, Diet 2: basal diet plus 20% ground flax seed, Diet 3: basal diet plus 4% flax hulls, Diet 4: basal diet plus 18% hot water extracted flax seed, Diet 5: basa diet plus 8% flaxseed oil. Diet 6: basal diet with a standard antibiotic (tylan).

To improve our knowledge of which bacteria are increased and decreased by antibiotic feeding, we proposed in 2003-04 to us CLI funds to generate cpn60 libraries of bacterial sequence data from the control diet and the antibiotic diet. Ms. Smith has prepared these libraries each containing 1200 clones. However, we have experienced delays in access to high throughput sequencing to obtain the sequence information from the libraries and conduct an analysis of colonization variation in pigs associated with antibiotic feeding. A report on these findings must therefore be delayed until the progress report in summer 2005. O note, as shown in figure 4, Flax hulls and flax oil (linseed oil) increased Lactobacillus counts in pig ileum in a manner similar to the antibiotic suggesting that theses fractions may have some probiotic value in improving pig health and performance.

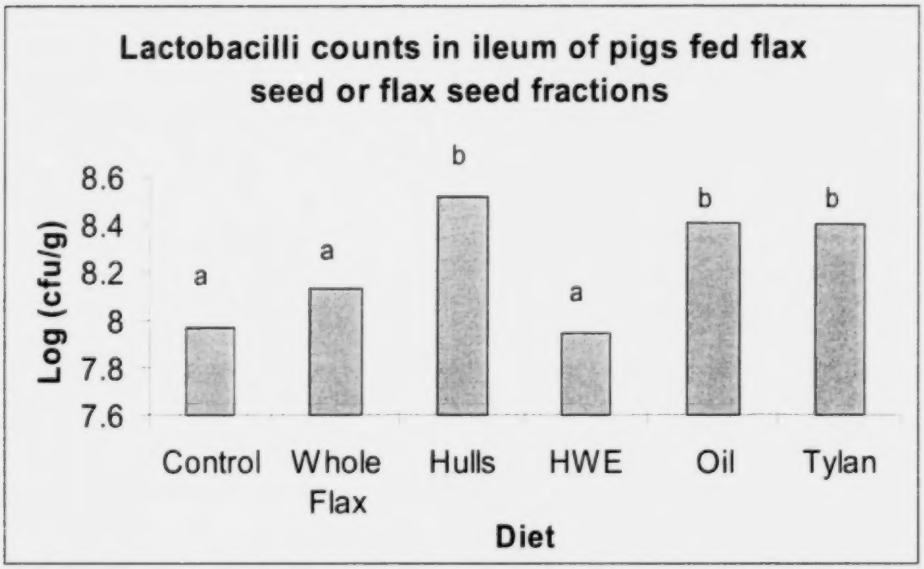


Figure 4. Flaxhulls and oil increased ileal lactobacilli plate counts similar to observed with the antibiotic diet. Bars with different letters are significantly ($P < 0.05$) different.

Lactobacilli enumerated by plate count represent a diverse group of species all of which likely do not behave identically in the gut and may or may not be beneficial to the pig. In advance of obtaining library results for the basal and antibiotic diets, we employed CLI funds to use molecular approaches to examine the abundance of 2 species of lactobacilli to determine whether the oil and hull fractions behaved similarly to antibiotic at the *Lactobacillus* spp. level. As shown in Figures 5 and 6, flax oil markedly increased *L. amylovorus,* the dominant lactobacilli in the pig, above that observed by antibiotic but unlike antibiotic, did not markedly increase *L. johnsonii*. Flax hulls on the other hand did not increase either of these lactobacilli suggesting that the increase in lactobacilli plate counts observed with hulls was due to another lactobacilli.

Figures 7 and 8 illustrate ileal colonization by *Clostridium perfringens* and *E. coli*. Ileal colonization by these potential pathogenic bacteria was not markedly affected by any of the diets although *C. perfringens* was lowest in the group fed flax oil.

Our results suggest potential health benefits in flax oil and hull fractions associated with modificed intestinal colonization in the pig. As a result we have obtained funding from SaskPork and ADF projects to continue and investigation of these fractions in a commercial setting.

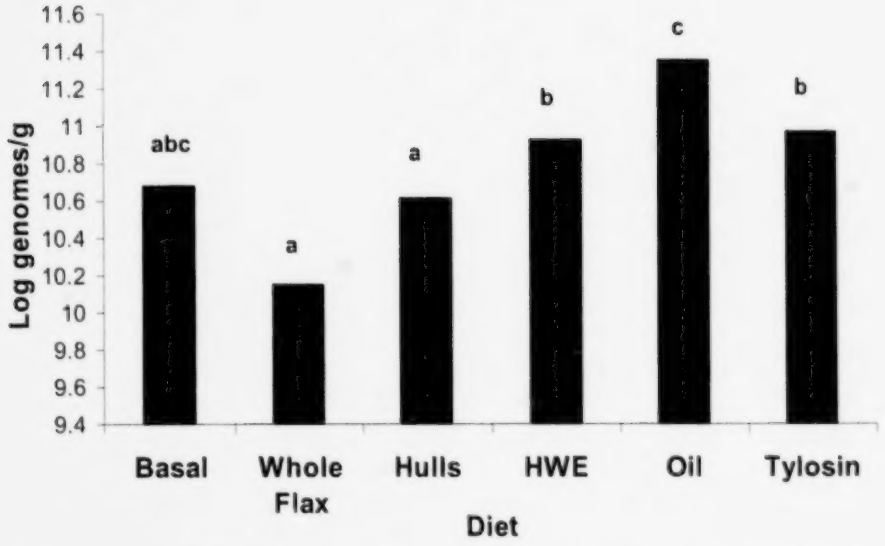


Figure 5. Mean log number of *Lactobacillus amylovorus* genomes detecting in ileum of pigs fed a basal diet plus antibiotic, wholeflax or flax fractions. Bars with different letters are significantly ($P < 0.05$) different.

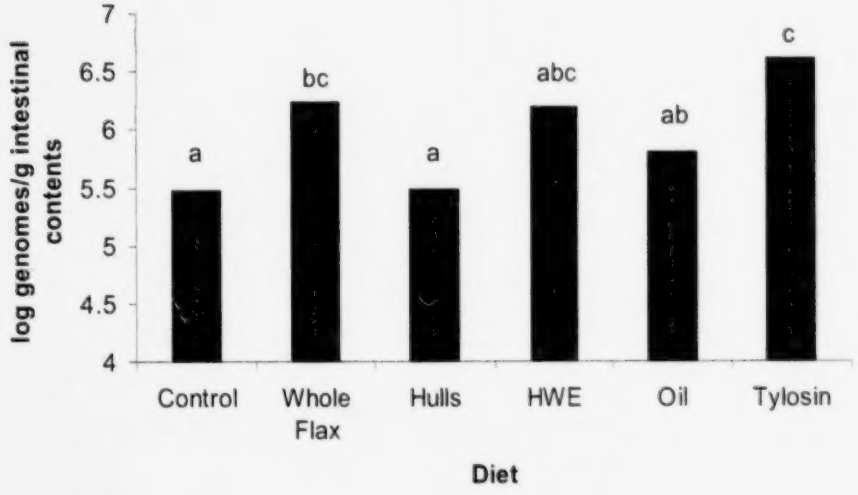


Figure 6. Mean log number of *Lactobacillus johnsonii* genomes detected in ileum of pigs fed a basal diet plus antibiotic, wholeflax or flax fractions. Bars with different letters are significantly ($P < 0.05$) different.

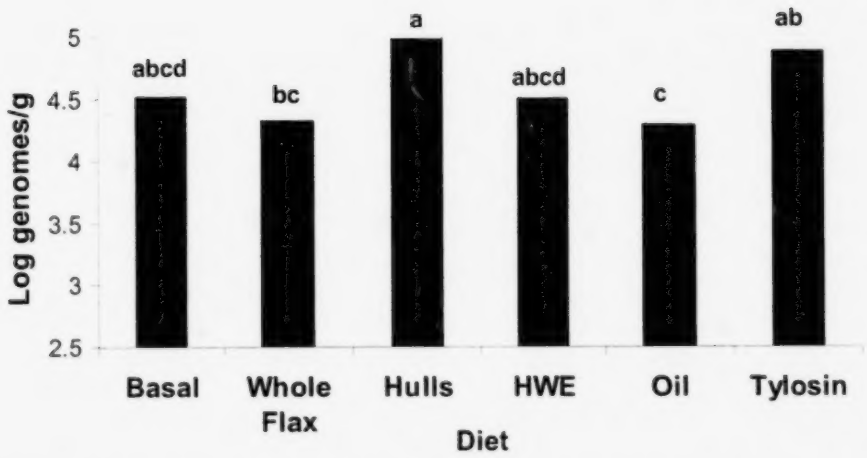


Figure 7. Mean log number of *Clostridium perfringens* genomes in ileal contents of pigs fed a basal diet plus antibiotic, wholeflax or flax fractions. Bars with different letters are significantly ($P < 0.05$) different.

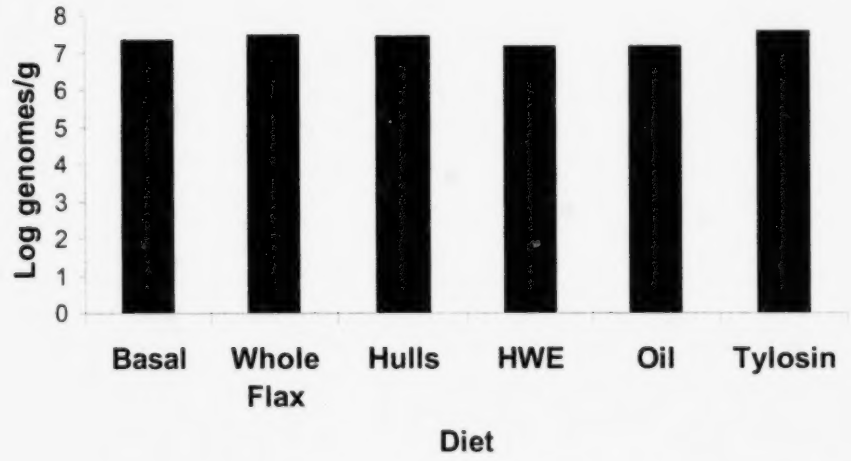


Figure 8. Mean log number of *Escherichia coli* genomes in ileal contents of pigs fed a basal diet plus antibiotic, wholeflax or flax fractions. Bars with different letters are significantly ($P < 0.05$) different.

3.7 Nitrogen cycling Saskatchewan crops in cattle.
This activity was not completed. Dr. Tim Mutsvangwa received ADF project funding for a similar proposal and felt that accepting funding from the Crops-Livestock Interface project for this work would be a conflict. An adjustment to the funding level of the project will be arranged with ADF.

4. Future Direction and Linkages

Our work plan for 2004-2005 is Attached as Appendix A.

5. Personnel

Tracey Kennedy, Graduate Student
Tanya Schafer, Graduate Student: Start May 1, 2004

6. Equipment. No equipment has been purchased or rented to this point.

7. Project Development Materials:

7.1 Feed Database All crop analyses are available through the Feed Database which is administered by Vern Racz.

7.2 Publications

L.F. Smith, R.T. Zijlstra, M.D. Drew, and A.G. Van Kessel. 2004. Effect of flaxseed fractions and sub-therapeutic antibiotic inclusion on microbial ecology in small intestine of growing pigs. J. Anim. Sci. 83(Suppl 1):140.

8. Project Photos. None available at this time.

9. Acknowledgment: The various publications will include acknowledgement of the Saskatchewan Agricultural Development Fund.

10. ICAR Data included previously.

APPENDIX A

Crops-Livestock Interface Feed Investigation Project

Proposed Work Plan for 2004-2005

Murray Drew[1], Peiqiang Yu[1], Brian Rossnagel[2] and Andrew Van Kessel[1]

[1]Department of Animal and Poultry Science, [2]Crop Development Centre
University of Saskatchewan

December 1, 2004

Introduction

We have two primary goals this year: 1) Develop a slow degradable starch variety of barley for swine and cattle and 2) Investigate the nutritional and antibacterial properties of flax fractions in pigs.

Activity 1: Development of a slow degradable starch variety of barley.

Activity 1a: Swine research.

Proposed Methods

Two experiments will be performed in 2004-2005. We will determine the starch degradation properties of 31 barley samples listed in Table 2 of this report in pigs using our in vivo method. This method has been described in detail in a previous report. This will allow us to select varieties with the slowest degradation rates for inclusion into a breeding program to develop a commercial slow starch degradable barley variety for Saskatchewan swine and beef producers. Additionally we will attempt to develop a variety with both slowly degradable starch and acceptable malting characteristics to allow growers to access both the malt and feed barley markets.

The second experiment will be to investigate the effect of feeding pigs slow starch degradable barley on amino acid utilization. Twelve barrow grower pigs (approximately 30 kg) will be fed isoenergetic diets formulated using extreme low and high glycemic index starch sources, based on results obtained from the previous two trials. The trial will consist of three experimental periods of 2 weeks each. Nine days will be required for acclimation to the test diets. There will be one period consisting of 5 days of total faecal and urine collection. Two blood samples per pig will be obtained on d 10 of each period. Four experimental diets will be processed. Dietary ingredients will consist of varieties of the same base grain barley consisting of either Valier (a slowly digestible starch) or Kendall (a rapidly digestible starch), as well as one of two levels of digestible lysine, 0.9 and 0.7 x NRC requirements for swine (limiting for amino acids), (NRC, 1998). Other indispensable amino acids will be adjusted to lysine based on ideal protein ratios. Barley will be ground to 900 µm. The isoenergetic diets will be formulated to contain the feed ingredients as the sole source of starch and energy in the diet, and balanced for Digestible Energy, amino acids and equal starch contents (Table 3). The feed will be provided to animals twice daily at a feeding level of 3.0 x maintenance for DE (NRC, 1998). Feed allowance will be calculated based on the body weight of each pig at the start of each experimental period, using the formula 3.0 (110 kcal x kg $BW^{0.75}$). Diets will be tested in a 2 x 2 factorial arrangement for a total of four treatments.

Faecal samples will be pooled over each collection period into one bag per pig, and stored in a freezer maintained at -20°C until analyses. Urine collection trays (1.5 x 1.5 m) will be installed underneath crates during collection periods. Urine will be collected in plastic containers via funnels beneath individual collection trays. Collected urine will be removed twice a day, weighed and stored at 4°C. A 5% aliquot will be taken and stored at -20°C until analyses. To

prevent volatilization of urinary N during collection and storage, 8 ml of 25% H_2SO_4 will be added to each container every day (Grala et al., 1997). On d 10, two blood samples will be collected from each pig via jugular venipuncture, before the morning feeding (0800) and 4 h postfeeding (1200). Blood will be centrifuged, and plasma will be frozen at -20°C (Zervas and Zijlstra, 2002), until analyses for glucose, insulin and urea.

Prior to experimentation, representative feed samples will be taken prior to each experimental period for analyses. Approximately 100 g of each diet will be ground to 1.0 mm for proximate analyses and amino acid profile, and 0.5 mm for total starch and free glucose analyses (Englyst et al., 1992).

Experimental factors that will be measured include plasma urea N, Total N ingested (Ni), Total N absorbed (Na), total N excreted in urine (Nu) and faeces (Nf) and total N retained (Nr), where:

Na = Ni - Nf

Nr = Ni - Nf- Nu

This experiment will support the marketing of a slow starch degradable barley variety to swine producers in Western Canada.

Significance of work:

This research will improve our ability to formulate diets for pigs resulting in improved efficiency of nutrient utilization, faster growth and improved carcass characteristics. Improved *in vitro* methods for predicting starch degradation and glycemic index in pigs will allow the rapid assessment of grain samples. In the longer term it will allow us to develop improved feed varieties of barley for swine and ruminants.

Activity 1b: Ruminant Research

Objectives:

Long-term: To screen the best variety of barley for ruminants and increase basic knowledge of the nutritional relevance of barley characteristics, structure and chemistry and to apply this information to the production of high quality feeding programs through plant breeding.

Short-term:

1. To determine digestive behavior and nutrient utilization of barley seeds in ruminants: COMPARISON of different varieties of barley seeds.

2. To predict nutrient supply to ruminants of barley seeds in ruminants: COMPARISON of different varieties of barley seeds.

3. To reveal ultrastructural-chemical features and makeup of barley seeds at a cellular level to help understand the relationship of complex intrinsic structures and matrix relative to barley nutritive quality,

nutrient utilization and digestive behavior in ruminants: COMPARISON of barley varieties
4. To provide information for barley breeding programs for selecting superior varieties of barley and for prediction of barley quality and nutritive value for humans and animals.

Literature Review, Research Motivation and Originality

Background: Barley varieties

Barley has an attractive energy and protein content compared to corn (Khorasani et al., 2000). It is high in starch (Yang et al., 1997a; 1997b) with a common A-type x-ray pattern (Robyt, 1998). Barley contains higher levels of lysine, methionine, tryptophan, and cystine than corn (Pond et al. 1995). In western Canada, barley is the primary constituent of concentrate rations for dairy and beef cattle. Differences in the nutritional characteristics among barley varieties have been reported (Molina-Cano et al., 1997; Khorasani et al., 2000; Yu et al., 2003b and 2004b). However, little research has been conducted to determine the magnitude of the differences between and within varieties of barley in terms of digestive behavior, nutrient utilization and potential nutrient supply to ruminant animals. In Saskatchewan, there are more than 30 varieties of barley are available. However, the detailed nutritive values for ruminants are not available in term of degradation kinetic, nutrient utilization and potentially nutrient supply.

Digestive behavior and nutrient availability of barley seeds in ruminants

Barley has particularly high starch (40-60%) and protein (12-15%) contents. However its rapid and extensive degradation and fast degradation rate (Kd) of dry matter (EDDM, 78%), protein (EDCP 91%) and starch (EDST 90%) by rumen microbes make them unsuitable (acidosis) and/or inefficient (unsynchronized) to be used as diets for high producing dairy cows or fast growing ruminants. High degradation rate and extend of barley (Nocek and Tamminga, 1991) may result in digestive disorders, bloat and acidosis (Ørskov, 1979; Givens et al., 1993) when feeding barley-based concentrate diets. Using DVE/OEB model estimates that barley (meal) has low truly digestive protein (94 g/kg DM) and negative degraded protein balance (-14 g/kg DM), which indicate microbial protein synthesis is predicted to be impaired (Yu et al., 2003b). Under certain condition, it is advantageous to have more starch and protein escape degradation in the rumen and provide a source of glucose and amino acid in the small intestine to achieve a higher milk production and fast growth rate. If barley is to be used more efficiently in high yielding dairy cows or growing ruminants (beef cattle), the extent of protein and starch degradation in the rumen must be reduced without negatively affecting their intestinal digestibility.

Different approaches have been made to attempt to reduce the extensive degradation rate and degradability and increase maximum nutrient availability (Yu et al., 2000 and 2002). One of approaches is through barley breeding program (Brian Rossnagal, Personal contact). Recently more then thirty varieties of barleys have been obtained by Crop Development Center (CDC, University of Saskatchewan). The objective is to screen and select the best variety of barley for ruminants in terms of nutrient utilization and availability.

Modeling nutrient supply to ruminants for barley seeds

To determine the differences in potential nutrient supply to ruminants among the different varieties of barley, modern nutrient evaluation systems are required. There are several sophisticated models have been developed, such as PDI (INRA, 1978; Vérité and Geay, 1987), ARC (1984), NJK-NJF (1985), AAT-PVB (Madsen, 1985), AP (NRC, 1985), ADPLS and MF (Varhegyi et al., 1998). Based on principles in existing nutrient evaluation models, modern nutrient evaluation systems: the DVE/OEB system (Tamminga et al., 1994) and NRC-2001 model (NRC, 2001) have been developed. These two models consider the strong elements of other recently developed protein evaluation systems and they also introduce new elements, such as the role of energy balance in intestinal protein supply. In the DVE/OEB system, the protein value are both expressed as the amount of protein (microbial and feed source) truly digested in and absorbed from the small intestine of the animal. This system can give information on the quantitative aspects of both ruminal and post-ruminal protein digestion in ruminants.

In the DVE/OEB system, each feed has a DVE value, which stands for true absorbable protein in the small intestine, composed of: 1) digestible feed true protein escaping rumen degradation; 2) digestible true microbial protein synthesized in the rumen, and 3) a correction for endogenous protein losses in the digestive tract. Each feed also has a rumen Degraded Protein Balance value, called OEB, which shows the (im)balance between microbial protein synthesis potentially possible from available rumen degradable protein and that potentially possible from the energy extracted during anaerobic fermentation in the rumen. When OEB is positive, it indicates the potential loss of N from the rumen. When negative, microbial protein synthesis may be impaired because of a shortage of N in the rumen. The optimum OEB value in a ration is therefore zero or slightly above (Tamminga et al., 1994). The NRC model (2001) introduced the concepts of metabolizable protein (MP), defined as true protein that is digested and absorbed by the intestine, and contributed by 1) ruminally undegraded feed CP, 2) ruminally synthesized microbial CP, and 3) endogenous CP from rumen. Based on the data from NRC model (NRC, 2001), the rumen Degraded Protein Balance can be calculated and it reflects the difference between the potential microbial protein synthesis based on ruminally degraded feed CP and that based on TDN as energy available for microbial fermentation in the rumen. The comparison between these two systems or model in prediction of nutrient supply from forages (Yu et al., 2003d) and concentrates (Yu et al., 2004f) has been reported. There two advanced models will be used to quantify nutrient supply from the barley seeds to distinguish the variety differences.

3.4. Using advanced synchrotron technology for nutrient matrix and interaction study of barley seeds at a cellular level

Traditional "wet" analytical chemistry usually looks for a specific known component through homogenization of the tissue and separation of the components of interest from the complex matrix. As a result, the information about the spatial origin and distribution of the component of interest is lost and the object of the analysis is destroyed (Budevska, 2002). Therefore using traditional "wet" chemical analysis, the barley inherent structure and nutrient matrix associated with nutritive value and digestive behavior are destroyed. Therefore traditional "wet" analytical chemistry fails to detect barely inherent structuralchemical features.

Synchrotron-based Fourier transform infrared microspectroscopy (SR-FTIR) has been developed as a rapid, direct, non-destructive and non-destructive analytical technique (Wetzel, 2001; Miller, 2002). This technique, which takes advantage of synchrotron light brightness, is capable of exploring the molecular chemistry within microstructures of biological tissues without destroying the inherent structure and matrix within cellular dimensions (Wetzel et al, 1998 and 1999; Wetzel, 2001; Marinkovic et al., 2002). It can generate spatially localized chemical information without the need to homogenize the sample as done in traditional "wet" analytical chemistry. Our previous studies (Yu, 2004d) showed that using the SR-FTIR technique, feed biological components (eg. lignin, protein, lipid, structural and non-structural carbohydrates as well as their ratios) in the plant tissues could be imaged within cellular dimensions (Yu et al., 2003a, 2003c, 2004a and 2004g). The implication from this study is that we can chemically define the intrinsic feed structure and compare feed materials (without destroying their structure) according to spectroscopic characteristics, functional groups, spatial distribution and chemical intensity. Chemical differences were identified in the ultrastructural matrix of endosperm tissue between Harrington (maltingtype) and Valier (feed-type) barley in relation to rumen degradation characteristics (Yu et al., 2004b). The greater association of the protein matrix with the starch granules in the endosperm tissue of Valier barley may limit access of ruminal microorganisms to the starch granules and thus reduce the rate and extent of rumen degradation relative to that of Harrington barley (Yu et al., 2003b and 2004b). It is the first time that the ultrastructural matrix in endosperm of barley could be revealed by using the novel SR-FTIR technique, which makes it possible to link barley intrinsic structures to nutrient utilization and digestive behavior in ruminants. Also, chemical features of protein (amide I) secondary structures of protein feed sources (oat, wheat, barley vs. feature) were quantified and highly related to feed protein values (Yu et al., 2004c). Our previous studies show that the advanced synchrotron-based analytical technique (SR-FTIR) can link plant intrinsic structures at a cellular level to nutrient utilization and can be used for feeds, feed chemistry and nutrition research (Yu et al., 2003c and

Yu, 2004d) and has tremendous potential to increase the fundamental understanding of plant structures at a cellular level.

Methodology and Proposed Approach

A series of experiments will be conducted to address each of the Objectives. Barley seeds will include 31 varieties obtained from CDC center, commonly grown in Western Canada. To determine digestive behaviour and nutrient utilization of barely seeds in ruminants: COMPARISON of varieties of barley seeds (**Objective 1**), in terms of in vitro total digestibility and in situ rumen degradation kinetics, these procedures will be followed: The rumen degradation kinetics and total digestion will be determined using the in situ and in vitro techniques with ruminally cannulated cattle. Total digestibility will be determined using modified Terry and Tilley in vitro method. Ruminal degradation kinetics will be determined using the in situ method as described in Yu et al. (2000 and 2003b). Incubation of all treatments in the rumen will be with 7 g dry matter in each nylon bag (5×7 cm) with the pore size of approximately 40 μm. The rumen incubations will be performed according to the 'gradual addition/all out' schedule. Samples will be incubated in the rumens for 0, 2, 4, 8, 12, and 24 h. Total bags for each treatment will be 12 bags. After incubation, the bags will be removed from rumen and washed with cool water without detergent and subsequently dried at 55°C for 48 h. The dry residues will be pooled according to treatments and incubation time for chemical analysis of dry matter, nitrogen, lipid, amino acids, starch and fibers. Rumen degradation parameters of each component will be estimated according to the first order kinetics model (Ørskov and McDonald, 1979). The ratios of degradation characteristics will be calculated (Tamminga et al., 1990; Yu et al., 2004e). To predict nutrient supply to ruminants of barley seeds in ruminants: COMPARISON of varieties of barley seeds (**Objective 2**), in terms of potentially nutrient supply, these procedures will be followed: Modeling nutrient supply of the barley samples will be used the NRC-2001 model (NRC, 2001) and DVE/OEB system (Tamminga et al., 1994), in terms of degraded protein balance and total truly absorbed protein in the small intestine (Yu et al., 2003d; Yu, 2004f). The degraded protein balance is the balance between microbial protein synthesis from rumen degradable protein and that from the energy extracted during anaerobic fermentation in the rumen. When the degraded protein balance is positive, it indicates the potential loss of N from the rumen. When negative, microbial protein synthesis may be impaired. Truly absorbed protein in the small intestine is contributed by a) feed protein escaping rumen degradation, b) microbial protein synthesized in the rumen and c) endogenous protein. To reveal ultrastructural-chemical features and makeup of barley at a cellular level in relation to nutritive quality, nutrient utilization and digestive behavior in ruminants (**Objective 2.2.4**), in terms of chemical bonding, functional groups and nutrient matrix /interaction (eg. protein matrix; distribution and intensity of protein to fibre ratio), these procedures will be followed: **1)** the barely seeds will be cut into thin cross sections (ca. 6 μm thickness) using a crystatic microtome. The unstained cross-sections of the tissues will be transferred to BaF_2 windows (size 13×1mm disk) for transmission mode in synchrotron transmission FTIR microspectroscopic work. The unstained cross-sections will be dry mounted onto Low-e IR microscope slides (Kevley Technologies) for reflectance mode in synchrotron transmission FTIR microspectroscopic work. **2)** The experiments will be performed at synchrotron center (NSLS or CLS) with synchrotron-based FTIR microspectroscopy. The spectroscopic mapping data will be recorded using a FTIR spectroscopy equipped with an IR microscope. The bench will be configured with a synchrotron light beamline. The spectra will be collected in the mid-IR range of 4000-800 cm^{-1} at a resolution of 4 cm^{-1} with 64 scans co-added. The aperture setting will be ca. 10×10 μm. The reasons for the chosen aperture size of 10×10 μm are: a) The size is within plant cellular dimension (plant cell size 5~30 μm); b). The 10×10 μm aperture size is the ideal for signal to noise ratio spectrum mapping of feed tissues. The mapping steps will be equal to aperture size. Scanned visible images will be obtained using a charge coupled device (CCD) camera linked to the IR images. **3)** The spectral data of the barley tissues will be collected and analyzed using the Bruker-OPUS or OMNIC software. The data will be displayed as either as a series of spectroscopic images collected at individual wavelengths, or as a

collection of IR spectra obtained at each pixel position in the image. Functional groups bands will be identified according to published literatures (Jackson and Mantsch, 1996 and 2000; Wetzel et al., 1998; Wetzel, 2003; Himmelsbach et al., 1998; Yu et al., 2003a and 2004b). Chemical imaging of functional groups will be determined by the OPUS or OMNIC software. The protein matrix in terms of the biological component ratio maps (eg. protein to starch ratio, protein to cellulose ratio) in the barley tissue will be determined by using peak ratio mapping function in the software. The peak ratio images will be obtained by the height or area under one functional group band (such as protein amide I 1650 cm^{-1}) divided by the height or area under another functional group band (such as starch 1025 cm^{-1}) at each pixel (pixel size 10×10 μm), which represents the biological component (protein to starch) ratio intensity and distribution in the tissue at a cellular level. The average component ratios (such as protein to starch) in the protein matrix will be calculated. When a biological component band has more or less interference with other bands, an agglomerative hierarchical cluster analysis (CLS) will be used to perform a cluster analysis of IR spectra data sets using the Cytospec software (Yu, 2004d).

Potential Impact of the Research and Expected Benefit

The information provided in this project may give better insight into the mechanisms and reasons of genotypic difference of barley affecting digestive behavior. The information may enable breeder to further improve the quality of barley and enable nutritionists, feed manufacturers and farmers to formulate rations, which could optimize rumen fermentation processes and reducing losses from the rumen fermentation process. From an ecological point of view, there is a benefit in reduced excess nutrient into soil water system, diminishing adverse affects on the environment, particularly in the dairy industry. Under circumstance, even a small improvement in the nutritive value of barley could be of significant economic consequence. It is anticipated that the proposed research program has tremendous potential that could influence and benefit the animal, feed and barley breeding industries.

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Activity 2: Gut microbiology and feed ingredients

General Hypothesis

The chemical composition of ingredients selected for use in animal diets significantly affects intestinal colonization by animal and human pathogens.

General Objectives:

1. To identify Saskatchewan feed ingredients or fractions thereof which improve pig health and reduce intestinal colonization by animal and human pathogens.

2. To compare intestinal microbial colonization, including (zoonotic) pathogen colonization among Saskatchewan feeds to identify varieties with beneficial animal health and/or food safety properties.

Workplan 2005-06

In evaluations of feed ingredients to date we have relied on enumeration of potential probiotic commensal bacteria and enumeration of (potential) pathogens present in research or commercial settings. Since increased probiotic populations such as lactobacilli are not a clear indicator of improved animal health/food safety and since pathogen populations are usually low and thus difficult to monitor and/or observe significant treatment differences, we propose to initiate a challenge model system to compare feed ingredients and varieties.

We propose to develop a *Salmonella cholerasuis* challenge model with guidance from Pre-harvest Food Safety Research Scientist Dr. Todd Calloway, ARS-USDA, College Station TX. Salmonella is the current #1 priority pathogen according to the US National Pork Board. The S. *cholerasuis* strain we will obtain from USDA causes morbidity (short term depression, reduction of intake and growth) in challenged pigs but not mortality. We will orally challenge "Trojan" pigs and after 6-12 hours place 1-2 of these challenged Trojan pigs in pens containing naïve pigs fed test diets. Growth rate, feed intake, rectal temperature and fecal shedding of Salmonella will be monitored in the naïve pigs to determine susceptibility transmission of Salmonella from the Trojan pigs. Figure 9 below is a result of our preparative work demonstrating that enrichment of pig feces in selenite cysteine broth can be used to give quantitative information of salmonella shedding even at low colonization rates. We will use of combination of enrichment and molecular enumeration to measure *S. cholerasuis* shedding in feces of Trojan-exposed pigs.

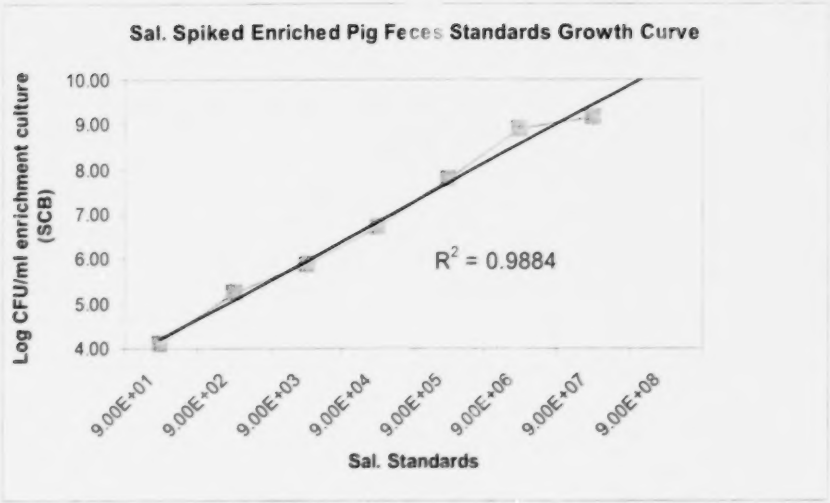

Figure 9. Mean log cfu/ml *Salmonella enteriditis* in fecal samples spiked with 90 to 90, 000 000 cfu *Salmonella enteriditis* and enriched for 7 hours in selenite cysteine broth (SCB). Results indicate enrichment can be used quantify Salmonella shedding at low levels in pig feces

Significance of Work

Reduced access to antibiotics in livestock agriculture is driving a requirement to identify alternative approaches to prophylactic control of animal pathogens and improved food safety. We and others (Pluske et al. 1998, Duirmic et al. 1998, Kontstantinov et al. 2003) have demonstrated that the source of feed ingredients (cereal grain, protein supplement) are major determinants of the profile of organism colonizing the digestive tract. Identification of flax fractions which reduce enteric infection in pigs will provide a new tool for Sasktachewan swine producers and a new market for processed SK flax.

Once developed, this model will be invaluable in comparing the health benefit of specific fractions of feed ingredients and optimum inclusion rates. In the 2005-06 budget year we request funds to develop a Salmonella challenge model in pigs and to assess the effect of flax fractions on transmission among pigs. In addition to the flax fractions described above a new emphasis will be focused on the mucilage fraction of flax hulls. Further fractionation of hulls will identify the active ingredient and allow higher inclusion rates of this active ingredient versus the entire hull.